

SEQUENCE LISTING



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<120> Human Receptor Proteins; Related Reagents and Methods

<130> DX0804

<140> 09/037,394

<141> 1998-03-09

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 1381

<212> DNA

<213> primate

<220>

<221> CDS

<222> (132)..(1064)

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TECH CENTER 1600/2900

<220>

<221> misc_feature

<222> n at position 567 and 573

<223> n may be A, C, T, or G; translated amino acid depends on genetic code

<400> 1

tcgacccacg cgtccgcgct gcgactcaga cctcagctcc aacatatgca ttctgaagaa 60

agatggctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaaact 120

gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170

Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr

1

5

10

agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca 218

Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr

15

20

25

gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca 266

Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser

30

35

40

45

acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga 314

Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly

50

55

60

gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg 362

Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu

65

70

75

tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa	410
Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu	
80 85 90	
ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac	458
Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr	
95 100 105	
aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc	506
Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser	
110 115 120 125	
atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct	554
Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro	
130 135 140	
ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag	602
Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu	
145 150 155	
gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag	650
Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu	
160 165 170	
cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca	698
Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro	
175 180 185	
gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc	746
Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala	
190 195 200 205	
cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca	794
Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr	
210 215 220	
gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg	842
Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu	
225 230 235	
ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc	890
Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe	
240 245 250	
gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg	938
Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val	
255 260 265	
gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc	986
Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile	
270 275 280 285	
agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct	1034
Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser	
290 295 300	
cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca	1084

Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
305 310

ggtgaagccg agaacctggt ctgcatgaca tggaaccat gaggggacaa gttgtgtttc 1144
tgttttccgc cacggacaag ggatgagaga agtaggaaga gcctgttgtc tacaagtcta 1204
gaagcaacca tcagaggcag ggtggtttgt ckaacagaac aaytgactga ggytakrggg 1264
gwtgtgacct ctagactktg ggstkscayt tgcwtggytg agcaaccctg ggaaaagtga 1324
cttcacccct tnggtccnaa gttttctcat ctgtaatggg ggatnccctac aaaactg 1381

<210> 2

<211> 311

<212> PRT

<213> primate

<220>

<221> misc_feature

<222> Xaa at residues 146, 148, 171, 214 and 225

<223> Xaa depends on corresponding codon

<400> 2

Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu Phe
1 5 10 15

Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val
20 25 30

Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met
35 40 45

Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val
50 55 60

Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser
65 70 75 80

His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu
85 90 95

Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg
100 105 110

Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys
115 120 125

His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu
130 135 140

Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly
145 150 155 160

Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala
165 170 175

Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu
 180 185 190

Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe
 195 200 205

Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val
 210 215 220

Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
 225 230 235 240

Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys
 245 250 255

Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro
 260 265 270

Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg
 275 280 285

Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu
 290 295 300

Leu Leu Arg Ala Trp Ile Ser
 305 310

<210> 3
 <211> 1244
 <212> DNA
 <213> primate

<220>
 <221> CDS
 <222> (2)..(694)

<400> 3
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tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc 97
 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
 20 25 30

tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc 145
 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
 35 40 45

ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay 193
 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
 50 55 60

tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac 241
 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn

65	70	75	80	
tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa	289			
Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln				
85	90	95		
gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc	337			
Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly				
100	105	110		
cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg	385			
Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr				
115	120	125		
aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg	433			
Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu				
130	135	140		
gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc	481			
Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly				
145	150	155	160	
ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc	529			
Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile				
165	170	175		
gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac	577			
Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp				
180	185	190		
aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt	625			
Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val				
195	200	205		
gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc	673			
Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr				
210	215	220		
caa aac tct ggt gcg gtc tgc tagcctgtgg ggtaagggct ctgagccgag	724			
Gln Asn Ser Gly Ala Val Cys				
225	230			
gaagctgctg atgtccatgt cagcacttta tggaatccgg tcttccattt tctgtcccc	784			
aaaaggccccg tcagtgcctg tgaagatgta acgggtctca tgggggagac aagcttattg	844			
atTTTTTTTct tcaaactaag agTTTTTctaa tcatacgctg ttttagaata attctacaga	904			
tatgtccccg aaagattaag atttctctta aacactaaaa agacatgtaa ttatttggtta	964			
gcaaattgggc gtctggcacg cctctgacac tttttcgta gcagccagga cagaggtcc	1024			
cctccttgat gaagcccctc gggcagacca tgtcacctgt ccagcctgc cccaagaagg	1084			
gacattaagt ggcccttctt catatccaaa cacctggctt gaaatgtgat tagccctgta	1144			
aatagtttca cagagattaa gcctTTTTTTT cccccaagtt aggaataaaa gactataatt	1204			

aacttttttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa

1244

<210> 4
<211> 231
<212> PRT
<213> primate

<220>
<221> misc_feature
<222> Xaa at residue 64
<223> Xaa translated amino acid depends on corresponding codon

<400> 4

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Trp	Phe	Leu	Ser	Cys	Trp	Asn	Val	Thr	Ile	Gly	Pro	Pro	Glu	Ser	Ile	
			20					25					30			
Trp	Val	Thr	Pro	Gly	Glu	Ala	Ser	Leu	Ile	Ile	Arg	Phe	Ser	Ser	Pro	
		35					40				45					
Phe	Asp	Val	Pro	Pro	Asn	Leu	Gly	Tyr	Phe	Gln	Tyr	Tyr	Val	His	Xaa	
	50					55				60						
Trp	Glu	Lys	Ala	Gly	Ile	Gln	Lys	Val	Lys	Gly	Pro	Phe	Lys	Ser	Asn	
	65				70					75					80	
Ser	Ile	Val	Leu	Asp	Gly	Leu	Arg	Pro	Leu	Arg	Glu	Tyr	Cys	Leu	Gln	
				85					90					95		
Val	Lys	Ala	His	Leu	Phe	Arg	Thr	Ser	Cys	Asn	Thr	Ser	Arg	Pro	Gly	
		100						105					110			
Arg	Leu	Ser	Asn	Ile	Thr	Cys	Tyr	Glu	Thr	Met	Met	Asp	Ala	Thr	Thr	
		115					120					125				
Lys	Leu	Gln	Gln	Val	Ile	Leu	Ile	Ala	Val	Gly	Val	Phe	Leu	Ser	Leu	
	130					135					140					
Ala	Ala	Leu	Ala	Gly	Gly	Cys	Phe	Phe	Leu	Val	Leu	Arg	Tyr	Lys	Gly	
	145				150					155					160	
Leu	Val	Lys	Tyr	Trp	Phe	His	Ser	Pro	Pro	Ser	Ile	Pro	Ser	Gln	Ile	
			165						170					175		
Glu	Glu	Tyr	Leu	Lys	Asp	Pro	Ser	Gln	Pro	Ile	Leu	Glu	Ala	Leu	Asp	
		180						185					190			
Lys	Asp	Thr	Ser	Pro	Thr	Asp	Asp	Ala	Trp	Asp	Leu	Val	Ser	Val	Val	
	195						200					205				
Ala	Phe	Pro	Ala	Lys	Glu	Gln	Glu	Asp	Val	Pro	Gln	Ser	Thr	Leu	Thr	
	210					215					220					

Gln Asn Ser Gly Ala Val Cys
225 230

<210> 5
<211> 337
<212> PRT
<213> primate

<400> 5

Met Arg Pro Thr Leu Leu Trp Ser Leu Leu Leu Leu Gly Val Phe
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Ala Ala Ala Ala Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala
20 25 30

Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser
35 40 45

Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Arg
50 55 60

Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met
65 70 75 80

Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe
85 90 95

Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr
100 105 110

Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr
115 120 125

Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu
130 135 140

Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser
145 150 155 160

Ser Pro Phe Asp Ile Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr
165 170 175

Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe
180 185 190

Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr
195 200 205

Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe
210 215 220

Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp
225 230 235 240

Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe
245 250 255

Ser Leu Leu Ser Val Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys
260 265 270

Tyr Arg Gly Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro
275 280 285

Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu
290 295 300

Ala Leu Asp Lys Asp Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val
305 310 315 320

Ser Ile Ile Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr
325 330 335

Leu

<210> 6
<211> 325
<212> PRT
<213> primate

<400> 6
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
1 5 10 15

Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
20 25 30

Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
35 40 45

Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
50 55 60

Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65 70 75 80

Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
85 90 95

His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
100 105 110

Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His
115 120 125

Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
130 135 140

Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145 150 155 160

Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu

165

170

175

Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
180 185 190

Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
195 200 205

Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala
210 215 220

Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly
225 230 235 240

Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe
245 250 255

Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His
260 265 270

Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu
275 280 285

Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser
290 295 300

Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly
305 310 315 320

Gln Gly Pro Gln Ser
325